



SEQUENCE LISTING

<110> WILEY, Steven R.

<120> TWEAK Receptor

<130> 2968-B

<140> US/09/742,454

<141> 2000-12-19

<150> 60/172,878

<151> 1999-12-20

<150> 60/203,347

<151> 2000-05-10

<160> 7

<170> PatentIn Ver. 2.0

<210> 1

<211> 898

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (52)..(873)

<220>

<223> Description of Artificial Sequence: human TWEAK
fusion protein construct

<400> 1

tctcgagggc cacgcgttta aacgtcgagg tacctatccc gggccgccac c atg gct 57
Met Ala
1

aca ggc tcc cgg acg tcc ctg ctc ctg gct ttt ggc ctg ctc tgc ctg 105
Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu Cys Leu
5 10 15

ccc tgg ctt caa gag ggc agt gca act agt tct gac cgt atg aaa cag 153
Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met Lys Gln
20 25 30

ata gag gat aag atc gaa gag atc cta agt aag att tat cat ata gag 201
Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His Ile Glu
35 40 45 50

aat gaa atc gcc cgt atc aaa aag ctg att ggc gag cgg act aga tct 249
Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr Arg Ser
55 60 65

agt ttg ggg agc cgg gca tcg ctg tcc gcc cag gag cct gcc cag gag 297
Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala Gln Glu

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<220>

<221> CDS

<222> (52)..(873)

<220>

<223> Description of Artificial Sequence: human TWEAK
fusion protein construct

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Met Ala Thr Gly Ser Arg Thr Ser Leu Leu Leu Ala Phe Gly Leu Leu
1 5 10 15

Cys Leu Pro Trp Leu Gln Glu Gly Ser Ala Thr Ser Ser Asp Arg Met
20 25 30

Lys Gln Ile Glu Asp Lys Ile Glu Glu Ile Leu Ser Lys Ile Tyr His
35 40 45

Ile Glu Asn Glu Ile Ala Arg Ile Lys Lys Leu Ile Gly Glu Arg Thr
50 55 60

Arg Ser Ser Leu Gly Ser Arg Ala Ser Leu Ser Ala Gln Glu Pro Ala
65 70 75 80

Gln Glu Glu Leu Val Ala Glu Glu Asp Gln Asp Pro Ser Glu Leu Asn
85 90 95

Pro Gln Thr Glu Glu Ser Gln Asp Pro Ala Pro Phe Leu Asn Arg Leu
100 105 110

Val Arg Pro Arg Arg Ser Ala Pro Lys Gly Arg Lys Thr Arg Ala Arg
115 120 125

Arg Ala Ile Ala Ala His Tyr Glu Val His Pro Arg Pro Gly Gln Asp
130 135 140

Gly Ala Gln Ala Gly Val Asp Gly Thr Val Ser Gly Trp Glu Glu Ala
145 150 155 160

Arg Ile Asn Ser Ser Ser Pro Leu Arg Tyr Asn Arg Gln Ile Gly Glu
165 170 175

Phe Ile Val Thr Arg Ala Gly Leu Tyr Tyr Leu Tyr Cys Gln Val His
180 185 190

Phe Asp Glu Gly Lys Ala Val Tyr Leu Lys Leu Asp Leu Leu Val Asp
195 200 205

Gly Val Leu Ala Leu Arg Cys Leu Glu Glu Phe Ser Ala Thr Ala Ala
210 215 220

Ser Ser Leu Gly Pro Gln Leu Arg Leu Cys Gln Val Ser Gly Leu Leu
225 230 235 240

Ala Leu Arg Pro Gly Ser Ser Leu Arg Ile Arg Thr Leu Pro Trp Ala
245 250 255

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His Leu Lys Ala Ala Pro Phe Leu Thr Tyr Phe Gly Leu Phe Gln Val
 260 265 270

His

<210> 3
 <211> 868
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (53)..(442)

<400> 3
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 Met Ala
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cgg ggc tcg ctg cgc cgg ttg ctg cgg ctc ctc gtg ctg ggg ctc tgg 106
 Arg Gly Ser Leu Arg Arg Leu Leu Arg Leu Leu Val Leu Gly Leu Trp
 5 10 15

ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc acc gcc 154
 Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly Thr Ala
 20 25 30

ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag tgc atg 202
 Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys Cys Met
 35 40 45 50

gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc ctg ggc 250
 Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys Leu Gly
 55 60 65

tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg ccc atc ctt 298
 Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro Ile Leu
 70 75 80

ggg ggc gct ctg agc ctg acc ttc gtg ctg ggg ctg ctt tct ggc ttt 346
 Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser Gly Phe
 85 90 95

ttg gtc tgg aga cga tgc cgc agg aga gag aag ttc acc acc ccc ata 394
 Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr Pro Ile
 100 105 110

gag gag acc ggc gga gag ggc tgc cca gct gtg gcg ctg atc cag tga 442
 Glu Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile Gln
 115 120 125

caatgtgccc cctgccagcc ggggctcgcc cactcatcat tcattcatcc attctagagc 502

cagtctctgc ctcccagacg cggcgggagc caagctcctc caaccacaag ggggggtgggg 562

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ggcgggtgaat cacctctgag gcctgggccc agggttcagg ggaaccttcc aaggtgtctg 622
 gttgccctgc ctctggctcc agaacagaaa gggagcctca cgctgggtca cacaaaacag 682
 ctgacactga ctaaggaact gcagcatttg cacaggggag gggggtgccc tccttcctag 742
 aggccctggg ggccaggctg acttgggggg cagacttgac actaggcccc actcactcag 802
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 agaggg 868

<210> 4
 <211> 129
 <212> PRT
 <213> Homo sapiens

<400> 4
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 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30
 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Thr Phe Val Leu Gly Leu Leu Ser
 85 90 95
 Gly Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110
 Pro Ile Glu Thr Gly Gly Glu Gly Cys Pro Ala Val Ala Leu Ile
 115 120 125
 Gln

<210> 5
 <211> 129
 <212> PRT
 <213> Mus sp.

<400> 5
 Met Ala Pro Gly Trp Pro Arg Ser Leu Pro Gln Ile Leu Val Leu Gly
 1 5 10 15
 Phe Gly Leu Val Leu Met Arg Ala Ala Ala Gly Glu Gln Ala Pro Gly
 20 25 30

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Thr Ser Pro Cys Ser Ser Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 Cys Met Asp Cys Ala Ser Cys Pro Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 Leu Gly Cys Ala Ala Ala Pro Pro Ala His Phe Arg Leu Leu Trp Pro
 65 70 75 80
 Ile Leu Gly Gly Ala Leu Ser Leu Val Leu Val Leu Ala Leu Val Ser
 85 90 95
 Ser Phe Leu Val Trp Arg Arg Cys Arg Arg Arg Glu Lys Phe Thr Thr
 100 105 110
 Pro Ile Glu Glu Thr Gly Gly Glu Gly Cys Pro Gly Val Ala Leu Ile
 115 120 125
 Gln

<210> 6
 <211> 932
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(930)
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 <223> Description of Artificial Sequence: human TWEAK
 receptor fusion protein construct

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 ctc tgg ctg gcg ttg ctg cgc tcc gtg gcc ggg gag caa gcg cca ggc 96
 Leu Trp Leu Ala Leu Leu Arg Ser Val Ala Gly Glu Gln Ala Pro Gly
 20 25 30
 acc gcc ccc tgc tcc cgc ggc agc tcc tgg agc gcg gac ctg gac aag 144
 Thr Ala Pro Cys Ser Arg Gly Ser Ser Trp Ser Ala Asp Leu Asp Lys
 35 40 45
 tgc atg gac tgc gcg tct tgc agg gcg cga ccg cac agc gac ttc tgc 192
 Cys Met Asp Cys Ala Ser Cys Arg Ala Arg Pro His Ser Asp Phe Cys
 50 55 60
 ctg ggc tgc gct gca gca cct cct gcc ccc ttc cgg ctg ctt tgg aga 240
 Leu Gly Cys Ala Ala Ala Pro Pro Ala Pro Phe Arg Leu Leu Trp Arg
 65 70 75 80
 tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc 288

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Ser	Cys	Asp	Lys	Thr 85	His	Thr	Cys	Pro	Pro 90	Cys	Pro	Ala	Pro	Glu 95	Ala	
gag	ggc	gcg	ccg	tca	gtc	ttc	ctc	ttc	ccc	cca	aaa	ccc	aag	gac	acc	336
Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	
			100					105					110			
ctc	atg	atc	tcc	cgg	acc	cct	gag	gtc	aca	tgc	gtg	gtg	gtg	gac	gtg	384
Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val	
		115					120					125				
agc	cac	gaa	gac	cct	gag	gtc	aag	ttc	aac	tgg	tac	gtg	gac	ggc	gtg	432
Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val	
	130					135					140					
gag	gtg	cat	aat	gcc	aag	aca	aag	ccg	cgg	gag	gag	cag	tac	aac	agc	480
Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser	
145				150				155							160	
acg	tac	cgt	gtg	gtc	agc	gtc	ctc	acc	gtc	ctg	cac	cag	gac	tgg	ctg	528
Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu	
			165					170					175			
aat	ggc	aag	gag	tac	aag	tgc	aag	gtc	tcc	aac	aaa	gcc	ctc	cca	gcc	576
Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala	
			180					185					190			
ccc	atc	gag	aaa	acc	atc	tcc	aaa	gcc	aaa	ggg	cag	ccc	cga	gaa	cca	624
Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro	
		195					200				205					
cag	gtg	tac	acc	ctg	ccc	cca	tcc	cgg	gag	gag	atg	acc	aag	aac	cag	672
Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln	
	210					215					220					
gtc	agc	ctg	acc	tgc	ctg	gtc	aaa	ggc	ttc	tat	ccc	agc	gac	atc	gcc	720
Val	Ser	Leu	Thr	Cys	Leu	Val	Lys	Gly	Phe	Tyr	Pro	Ser	Asp	Ile	Ala	
225				230				235							240	
gtg	gag	tgg	gag	agc	aat	ggg	cag	ccg	gag	aac	aac	tac	aag	acc	acg	768
Val	Glu	Trp	Glu	Ser	Asn	Gly	Gln	Pro	Glu	Asn	Asn	Tyr	Lys	Thr	Thr	
			245					250					255			
cct	ccc	gtg	ctg	gac	tcc	gac	ggc	tcc	ttc	ttc	ctc	tat	agc	aag	ctc	816
Pro	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser	Lys	Leu	
		260						265					270			
acc	gtg	gac	aag	agc	agg	tgg	cag	cag	ggg	aac	gtc	ttc	tca	tgc	tcc	864
Thr	Val	Asp	Lys	Ser	Arg	Trp	Gln	Gln	Gly	Asn	Val	Phe	Ser	Cys	Ser	
		275					280				285					
gtg	atg	cat	gag	gct	ctg	cac	aac	cac	tac	acg	cag	aag	agc	ctc	tcc	912
Val	Met	His	Glu	Ala	Leu	His	Asn	His	Tyr	Thr	Gln	Lys	Ser	Leu	Ser	
	290					295					3					

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<210> 7

<211> 309

<212> PRT

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(930)

<220>

<223> Description of Artificial Sequence: human TWEAK
receptor fusion protein construct

<400> 7

Met	Ala	Arg	Gly	Ser	Leu	Arg	Arg	Leu	Leu	Arg	Leu	Leu	Val	Leu	Gly
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Leu	Trp	Leu	Ala	Leu	Leu	Arg	Ser	Val	Ala	Gly	Glu	Gln	Ala	Pro	Gly
		20					25						30		

Thr	Ala	Pro	Cys	Ser	Arg	Gly	Ser	Ser	Trp	Ser	Ala	Asp	Leu	Asp	Lys
		35					40					45			

Cys	Met	Asp	Cys	Ala	Ser	Cys	Arg	Ala	Arg	Pro	His	Ser	Asp	Phe	Cys
	50					55					60				

Leu	Gly	Cys	Ala	Ala	Ala	Pro	Pro	Ala	Pro	Phe	Arg	Leu	Leu	Trp	Arg
65					70					75					80

Ser	Cys	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Ala
				85				90						95	

Glu	Gly	Ala	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr
		100						105					110		

Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	Val
	115						120					125			

Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	Gly	Val
	130					135					140				

Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	Tyr	Asn	Ser
145					150					155					160

Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	Gln	Asp	Trp	Leu
			165						170					175	

Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	Lys	Ala	Leu	Pro	Ala
		180						185					190		

Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	Gly	Gln	Pro	Arg	Glu	Pro
	195						200					205			

Gln	Val	Tyr	Thr	Leu	Pro	Pro	Ser	Arg	Glu	Glu	Met	Thr	Lys	Asn	Gln
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210

215

220

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
225 230 235 240

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
245 250 255

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu
260 265 270

Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser
275 280 285

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
290 295 300

Leu Ser Pro Gly Lys
305

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